LOADING ALL LIBRARIES

In [1]:
```
import os
import tensorflow as tf
import xml.etree.ElementTree
import numpy as np
import pandas as pd
import re
import matplotlib.pyplot as plt
from IPython.display import Image
from PIL import Image
from numpy import array
import string
import os
from PIL import Image
import glob
import pickle
from pickle import dump, load
from time import time
from keras.preprocessing import sequence
from keras.models import Sequential
from keras.layers import LSTM, Embedding, TimeDistributed, Dense, RepeatVector
,\
                         Activation, Flatten, Reshape, concatenate, Dropout, B
atchNormalization
from keras.optimizers import Adam, RMSprop
from keras.layers.wrappers import Bidirectional
from keras.layers.merge import add
from keras.applications.inception_v3 import InceptionV3
from keras.preprocessing import image
from keras.models import Model
from keras import Input, layers
from keras import optimizers
from keras.applications.inception_v3 import preprocess_input
from keras.preprocessing.text import Tokenizer
from keras.preprocessing.sequence import pad_sequences
from keras.utils import to_categorical
from sklearn.model_selection import train_test_split
from tqdm import tqdm
```

```
C:\Users\venka\Anaconda3\lib\site-packages\numpy\_distributor_init.py:32: Use
rWarning: loaded more than 1 DLL from .libs:
C:\Users\venka\Anaconda3\lib\site-packages\numpy\.libs\libopenblas.NOIJJG62EM
ASZI6NYURL6JBKM4EVBGM7.gfortran-win_amd64.dll
C:\Users\venka\Anaconda3\lib\site-packages\numpy\.libs\libopenblas.WCDJNK7YVM
PZQ2ME2ZZHJJRJ3JIKNDB7.gfortran-win_amd64.dll
  stacklevel=1)
Using TensorFlow backend.
```

```
In [2]: import numpy as np
        import pandas as pd
        import matplotlib.pyplot as plt
        import seaborn as sns
        from tqdm import tqdm
        import xml.etree.ElementTree as ET
        import os
        import cv2
        import tensorflow as tf
        from wordcloud import WordCloud
        import re
        from collections import defaultdict
        import itertools
        from collections import Counter
```

GETTING DATA FROM XML FILES

```
In [3]: #DATA FOLDER
        directory = r'ecgen-radiology'
```

```
In [4]: # extracting data from the xml documents
        #https://www.geeksforgeeks.org/xml-parsing-python/
        image = []
        impression = []
        img_finding = []
        for filename in tqdm(os.listdir(directory)):
            if filename.endswith(".xml"):
                f = directory + '/' + filename
                tree = ET.parse(f)
                root = tree.getroot()
                for child in root:
                    if child.tag == 'MedlineCitation':
                        for attr in child:
                            if attr.tag == 'Article':
                                for i in attr:
                                    if i.tag == 'Abstract':
                                        for name in i:
                                            if name.get('Label') == 'FINDINGS':
                                                finding=name.text

                for p_image in root.findall('parentImage'):

                    image.append(p_image.get('id'))
                    img_finding.append(finding)
```

```
100%|██████████████████████████████████████████████████████████████████████
████| 3955/3955 [00:01<00:00, 3928.28it/s]
```

In [5]:
```
#Storing the findings and image names in a data frame
Dataset = pd.DataFrame()
Dataset['Image_names'] = image
Dataset['Finding'] = img_finding
```

In [6]:
```
print(Dataset.shape)
Dataset.head()
```

```
(7470, 2)
```

Out[6]:

	Image_names	Finding
0	CXR1_1_IM-0001-3001	The cardiac silhouette and mediastinum size ar...
1	CXR1_1_IM-0001-4001	The cardiac silhouette and mediastinum size ar...
2	CXR10_IM-0002-1001	The cardiomediastinal silhouette is within nor...
3	CXR10_IM-0002-2001	The cardiomediastinal silhouette is within nor...
4	CXR100_IM-0002-1001	Both lungs are clear and expanded. Heart and m...

In [7]:
```
def abs_path(x):
    '''Makes the path absolute '''
    x = r'x ray data/'+ x + '.png'
    return x
```

In [8]:
```
Dataset['Image_names'] = Dataset['Image_names'].apply(lambda x : abs_path(x))
# making the paths absolute
```

In [9]:
```
Dataset.head()
```

Out[9]:

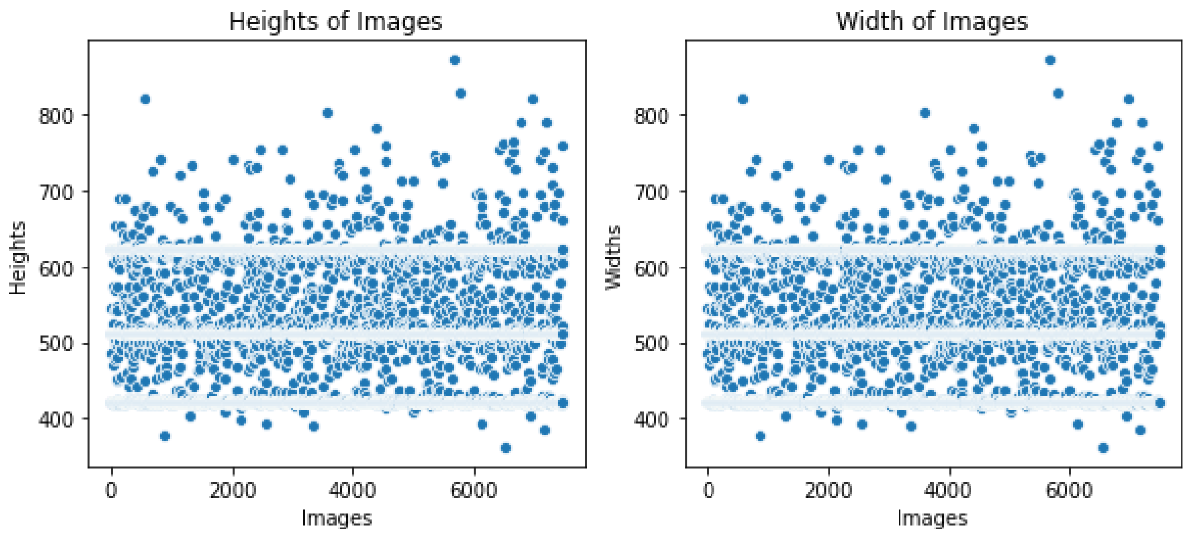
	Image_names	Finding
0	x ray data/CXR1_1_IM-0001-3001.png	The cardiac silhouette and mediastinum size ar...
1	x ray data/CXR1_1_IM-0001-4001.png	The cardiac silhouette and mediastinum size ar...
2	x ray data/CXR10_IM-0002-1001.png	The cardiomediastinal silhouette is within nor...
3	x ray data/CXR10_IM-0002-2001.png	The cardiomediastinal silhouette is within nor...
4	x ray data/CXR100_IM-0002-1001.png	Both lungs are clear and expanded. Heart and m...

In [10]:
```
# Loading the heights and widths of each image
h = []
w = []
for i in tqdm(np.unique(Dataset['Image_names'].values)):
    image = cv2.imread(i)
    h.append(image.shape[0])
    w.append(image.shape[1])
```

```
100%|████████████████████████████████████████
█████| 7470/7470 [00:24<00:00, 306.61it/s]
```

```
In [11]: #plotting the heights and widths of images
         plt.figure(figsize=(10,4))
         plt.subplot(121)
         plt.xlabel('Images')
         plt.ylabel('Heights')
         plt.title('Heights of Images')
         sns.scatterplot(range(len(h)), h)
         plt.subplot(122)
         plt.xlabel('Images')
         plt.ylabel('Widths')
         plt.title('Width of Images')
         sns.scatterplot(range(len(w)), h)

Out[11]: <matplotlib.axes._subplots.AxesSubplot at 0x18da1ee0fd0>
```



The Heights and widths are not same for all the images

PREPROCESSING IMAGE DATA

```
In [12]: print('Total Images:', Dataset['Image_names'].nunique())

         Total Images: 7470

In [13]: # checking for missing values
         Dataset.isnull().sum()

Out[13]: Image_names      0
         Finding        997
         dtype: int64

In [14]: # drop all missing value rows
         Dataset = Dataset.dropna(axis=0)
```

```
In [15]: Dataset.isnull().sum()

Out[15]: Image_names    0
         Finding        0
         dtype: int64
```

```
In [16]: print('Shape after preprocessing', Dataset.shape)

         Shape after preprocessing (6473, 2)
```

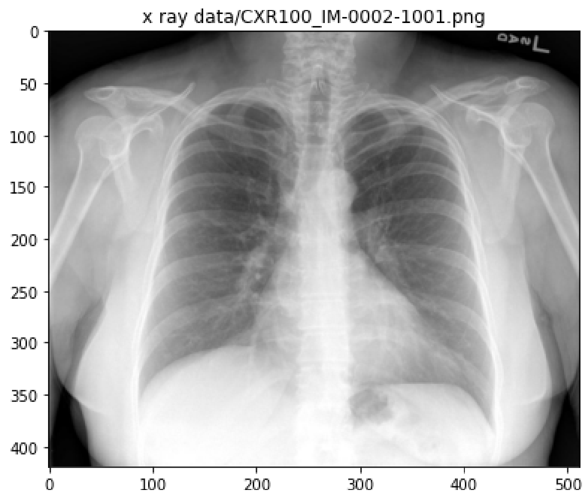
```
In [17]: Dataset.head(10)
```

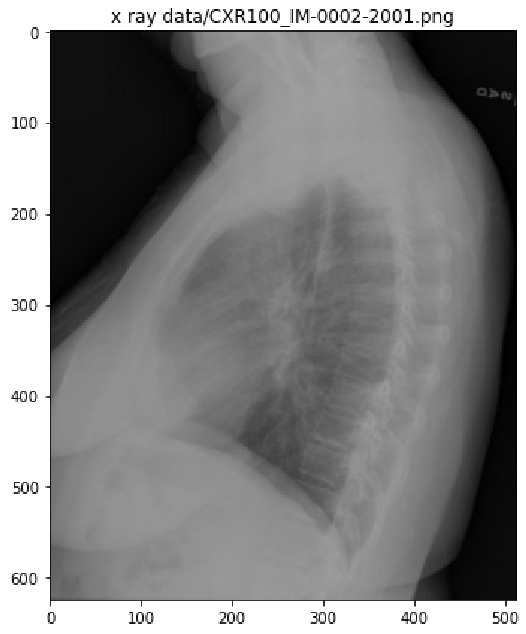
Out[17]:

	Image_names	Finding
0	x ray data/CXR1_1_IM-0001-3001.png	The cardiac silhouette and mediastinum size ar...
1	x ray data/CXR1_1_IM-0001-4001.png	The cardiac silhouette and mediastinum size ar...
2	x ray data/CXR10_IM-0002-1001.png	The cardiomediastinal silhouette is within nor...
3	x ray data/CXR10_IM-0002-2001.png	The cardiomediastinal silhouette is within nor...
4	x ray data/CXR100_IM-0002-1001.png	Both lungs are clear and expanded. Heart and m...
5	x ray data/CXR100_IM-0002-2001.png	Both lungs are clear and expanded. Heart and m...
6	x ray data/CXR1000_IM-0003-1001.png	There is XXXX increased opacity within the rig...
7	x ray data/CXR1000_IM-0003-2001.png	There is XXXX increased opacity within the rig...
8	x ray data/CXR1000_IM-0003-3001.png	There is XXXX increased opacity within the rig...
9	x ray data/CXR1001_IM-0004-1001.png	Interstitial markings are diffusely prominent ...

In [18]:
```
#printing images of two points
plt.figure(figsize=(14,7))
plt.subplot(121)
img1 = cv2.imread(Dataset['Image_names'].values[4])
plt.imshow(img1)
plt.title(Dataset['Image_names'].values[4])
plt.subplot(122)
img2 = cv2.imread(Dataset['Image_names'].values[5])
plt.title(Dataset['Image_names'].values[5])
plt.imshow(img2)
```

Out[18]:
```
<matplotlib.image.AxesImage at 0x18da232d748>
```





In [19]:
```
#printing findings of two points
Dataset['Finding'].values[4], Dataset['Finding'].values[5]
```

Out[19]:
```
('Both lungs are clear and expanded. Heart and mediastinum normal.',
 'Both lungs are clear and expanded. Heart and mediastinum normal.')
```

Here we see that two reports are same and the above images are also same but with a different angle.So we need to find images and reports like this.

In [20]:
```
# we are creating two dictionaries with image id and number of times it is pre
sent in dataset and findings of each report.
images = {}
findings = {}
for image, find in Dataset.values:
    i = image.split('-')#splitting the image at '-'
    i.pop(len(i)-1)#removing the numbers after - to find the x rays of same pa
tient
    i = '-'.join(e for e in i)
    if i not in images.keys():
        images[i] = 1
        findings[i] = find
    else:
        images[i] += 1
        findings[i] = find
```

In [22]:
```
images[r'x ray data/CXR1001_IM-0004'], findings[r'x ray data/CXR1001_IM-0004']
```

Out[22]:
```
(2,
 'Interstitial markings are diffusely prominent throughout both lungs. Heart
size is normal. Pulmonary XXXX normal.')
```

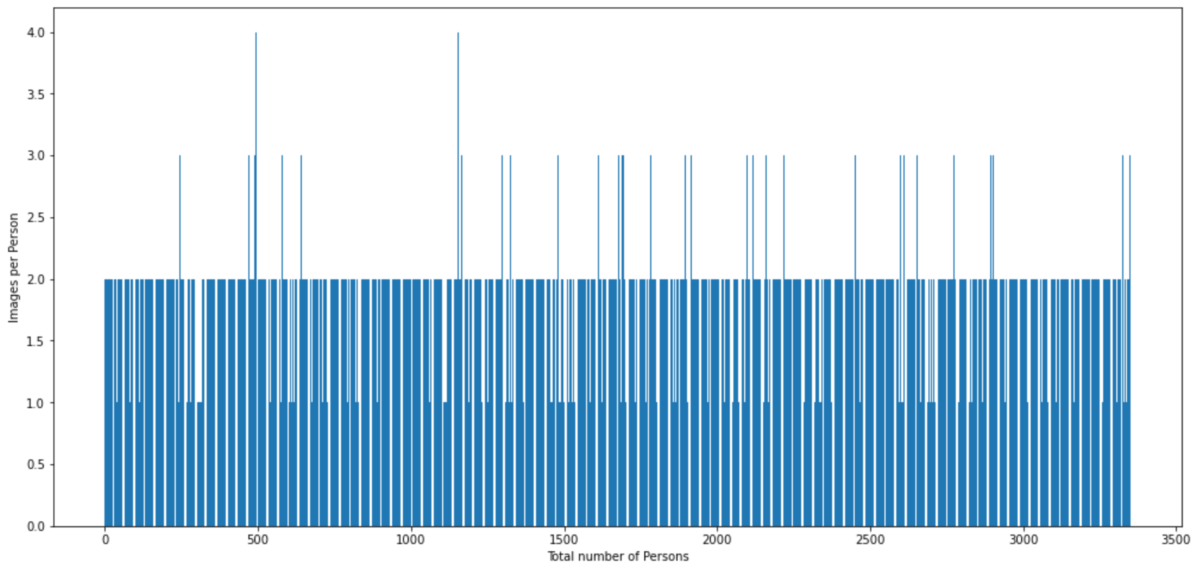
In [23]:
```
print('Total Number of unique images:', len(images.keys()))
```

```
Total Number of unique images: 3350
```

Here we can see that there are about 3350 unique images present in the dataset

In [24]:
```
#plotting a bar plot to see how many images we have per each person
plt.figure(figsize=(17,8))
plt.bar(range(len(images.keys())), images.values())
plt.xlabel('Total number of Persons')
plt.ylabel('Images per Person')
```

Out[24]:
```
Text(0, 0.5, 'Images per Person')
```



In [25]:
```
one = 0
two = 0
three = 0
four = 0
for i in images.values():
    if i == 1:
        one +=1
    elif i == 2:
        two += 1
    elif i == 3:
        three += 1
    elif i == 4:
        four += 1
    else:
        print('Error')
print(one, two, three, four)
```

```
390 2807 143 10
```

Here We can see that majority of people have 2 images and 4 being maximum only 10 people have 4 images.

In [26]:
```
len(images)
```

Out[26]:
```
3350
```

SPLITTING THE DATA

In [27]:
```
Data = list(images.keys())
Data_train = Data[:2500]
Data_cv = Data[2500:3000]
Data_test = Data[3000:3350]
```

In [28]:
```
def combining_images(images):

    image_per_person = defaultdict(list)  # creating a list of dictionary to s
tore all the image paths
                                              #corresponding to a person_id
    for pid in images:
        for img in Dataset['Image_names'].values:
            if pid in img:
                image_per_person[pid].append(img)
            else:
                continue
    return image_per_person
```

In [29]:
```
img_train = combining_images(Data_train)
img_cv = combining_images(Data_cv)
img_test = combining_images(Data_test)
```

In [30]:
```
len(img_train), len(Data_train)
```
Out[30]:
```
(2500, 2500)
```

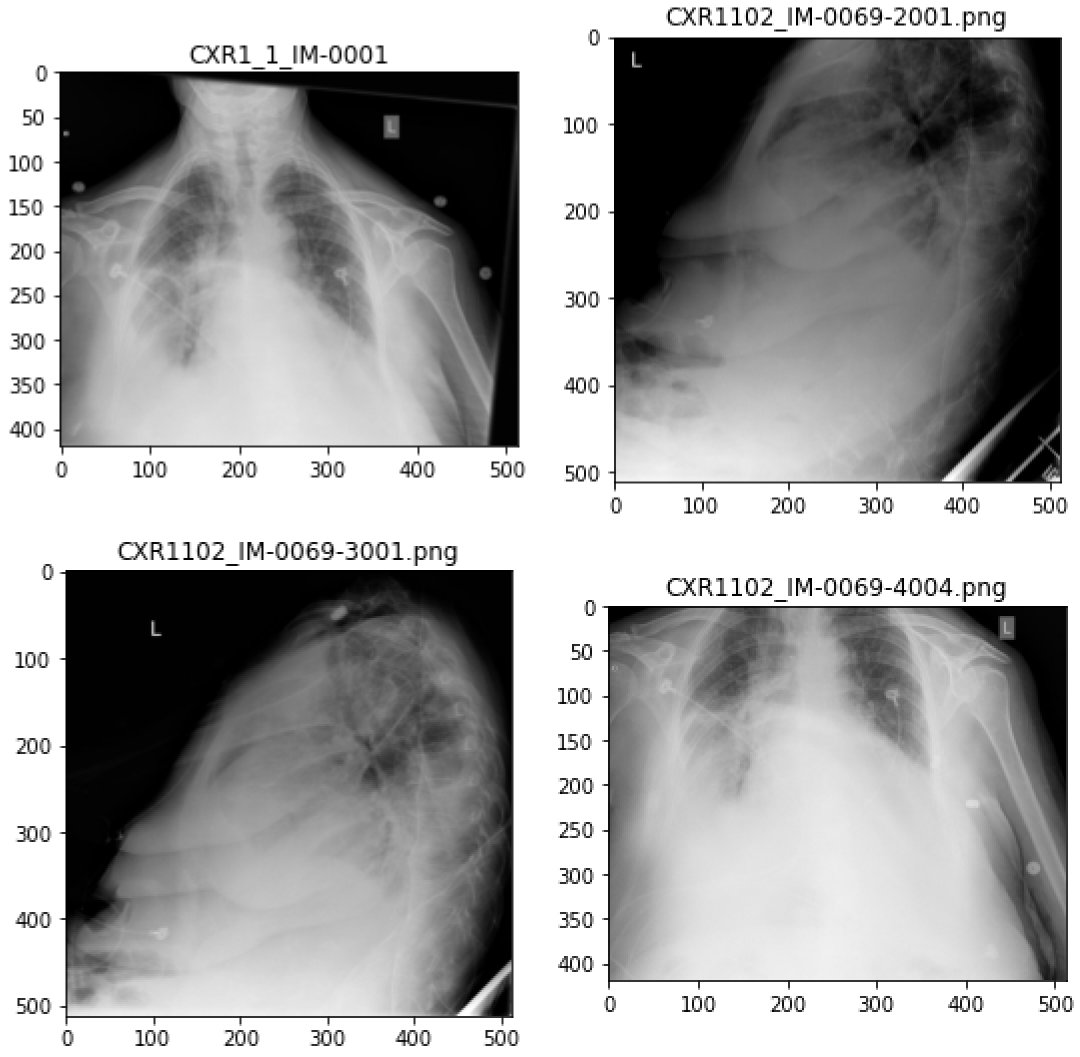
In [31]:
```
img_train['x ray data/CXR1_1_IM-0001']
```
Out[31]:
```
['x ray data/CXR1_1_IM-0001-3001.png', 'x ray data/CXR1_1_IM-0001-4001.png']
```

In [32]:
```
def load_image(file):
    img = tf.io.read_file(file)
    img = tf.image.decode_png(img, channels=3)
    img = tf.image.convert_image_dtype(img, tf.float32)
    return img
```

In [33]:
```
# checking which points have 4 images
for k,v in images.items():
    if v == 4:
        print(k)
        break
```
```
x ray data/CXR1102_IM-0069
```

```
In [36]: #plotting the four images of the point
         plt.figure(figsize=(9,9))
         plt.subplot(221)
         plt.imshow(load_image(r'C:\Users\venka\OneDrive\Desktop\cs2\x ray data/CXR1102
         _IM-0069-12012.png'))
         plt.title('CXR1_1_IM-0001')
         plt.subplot(222)
         plt.imshow(load_image(r'C:\Users\venka\OneDrive\Desktop\cs2\x ray data/CXR1102
         _IM-0069-2001.png'))
         plt.title('CXR1102_IM-0069-2001.png')
         plt.subplot(223)
         plt.imshow(load_image(r'C:\Users\venka\OneDrive\Desktop\cs2\x ray data/CXR1102
         _IM-0069-3001.png'))
         plt.title('CXR1102_IM-0069-3001.png')
         plt.subplot(224)
         plt.imshow(load_image(r'C:\Users\venka\OneDrive\Desktop\cs2\x ray data/CXR1102
         _IM-0069-4004.png'))
         plt.title('CXR1102_IM-0069-4004.png')
```

```
Out[36]: Text(0.5, 1.0, 'CXR1102_IM-0069-4004.png')
```



We have same scan in different angleslike front and sides.We have points with 1,2,3,4 scans per person in which majority have 2 scans.So we can take pair of Images as input to generate findings and The points with 1 scan can be augmented with same scan to have 2 scans for it.

CREATING FINAL DATA

In [37]:
```
def final_data(image_per_person):
    # new dataset
    Person_id, image_1, image_2, Findings = [],[],[],[]
    for pid, imgs in image_per_person.items():   #contains pid and the images
 associated with that pid

        if len(imgs) == 1:
            image_1.append(imgs[0])
            image_2.append(imgs[0])
            Person_id.append(pid)
            Findings.append(findings[pid])
        else:
            num = 0
            a = itertools.combinations(imgs, 2)
            for i in a:
                image_1.append(i[0])
                image_2.append(i[1])
                Person_id.append(pid + '_' + str(num))
                Findings.append(findings[pid])
                num += 1
    data = pd.DataFrame()
    data['Person_id'] = Person_id
    data['Image-1'] = image_1
    data['Image-2'] = image_2
    data['Findings'] = Findings

    return data
```

In [38]:
```
Train_data = final_data(img_train)
Test_data = final_data(img_test)
CV_Data = final_data(img_cv)
```

In [39]:
```
print(Train_data.shape)
print(Test_data.shape)
print(CV_Data.shape)
```

```
(2758, 4)
(399, 4)
(550, 4)
```

```
In [40]: Train_data.head()
```

Out[40]:

	Person_id	Image-1	Image-2	Findings
0	x ray data/CXR1_1_IM-0001_0	x ray data/CXR1_1_IM-0001-3001.png	x ray data/CXR1_1_IM-0001-4001.png	The cardiac silhouette and mediastinum size ar...
1	x ray data/CXR10_IM-0002_0	x ray data/CXR10_IM-0002-1001.png	x ray data/CXR10_IM-0002-2001.png	The cardiomediastinal silhouette is within nor...
2	x ray data/CXR100_IM-0002_0	x ray data/CXR100_IM-0002-1001.png	x ray data/CXR100_IM-0002-2001.png	Both lungs are clear and expanded. Heart and m...
3	x ray data/CXR1000_IM-0003_0	x ray data/CXR1000_IM-0003-1001.png	x ray data/CXR1000_IM-0003-2001.png	There is XXXX increased opacity within the rig...
4	x ray data/CXR1000_IM-0003_1	x ray data/CXR1000_IM-0003-1001.png	x ray data/CXR1000_IM-0003-3001.png	There is XXXX increased opacity within the rig...

TEXT PREPROCESSING

In [41]:
```
#https://www.kdnuggets.com/2018/03/text-data-preprocessing-walkthrough-python.
html
def lowercase(text):
    '''Converts to lowercase'''
    new_text = []
    for line in text:
        new_text.append(line.lower())
    return new_text

def decontractions(text):
    '''Performs decontractions in the doc'''
    new_text = []
    for phrase in text:
        phrase = re.sub(r"won't", "will not", phrase)
        phrase = re.sub(r"can\'t", "can not", phrase)
        phrase = re.sub(r"couldn\'t", "could not", phrase)
        phrase = re.sub(r"shouldn\'t", "should not", phrase)
        phrase = re.sub(r"wouldn\'t", "would not", phrase)
        # general
        phrase = re.sub(r"n\'t", " not", phrase)
        phrase = re.sub(r"\'re", " are", phrase)
        phrase = re.sub(r"\'s", " is", phrase)
        phrase = re.sub(r"\'d", " would", phrase)
        phrase = re.sub(r"\'ll", " will", phrase)
        phrase = re.sub(r"\'t", " not", phrase)
        phrase = re.sub(r"\'ve", " have", phrase)
        phrase = re.sub(r"\'m", " am", phrase)
        phrase = re.sub(r"\*+", "abuse", phrase)
        new_text.append(phrase)

    return new_text

def rem_punctuations(text):
    '''Removes punctuations'''
    punctuations = '''!()-[]{};:'"\,<>/?@#$%^&*~''' # full stop is not removed
    new_text = []
    for line in text:
        for char in line:
            if char in punctuations:
                line = line.replace(char, "")
        new_text.append(' '.join(e for e in line.split()))
    return new_text

def rem_numbers(text):
    '''Removes numbers and irrelevant text like xxxx*'''
    new_text = []
    for line in text:
        temp = re.sub(r'x*','',line)
        new_text.append(re.sub(r'\d','',temp))
    return new_text

def words_filter(text):
    '''Removes words less than 2 characters except no and ct'''
    new_text = []
    for line in text:
        temp = line.split()
        temp2 = []
        for word in temp:
            if  len(word) <=2 and word != 'no' and word != 'ct':
                continue
            else:
                temp2.append(word)
        new_text.append(' '.join(e for e in temp2))
    return new_text

def multiple_fullstops(text):
    ''' Removes multiple full stops from the text'''
    new_text = []
    for line in text:
        new_text.append(re.sub(r'\.\.+', '.', line))
    return new_text

def fullstops(text):
    new_text = []
    for line in text:
        new_text.append(re.sub('\.', ' .', line))
    return new_text

def multiple_spaces(text):
    new_text = []
    for line in text:
        new_text.append(' '.join(e for e in line.split()))
    return new_text

def separting_startg_words(text):
    new_text = []
    for line in text:
        temp = []
        words = line.split()
        for i in words:
            if i.startswith('.') == False:
                temp.append(i)
            else:
                w = i.replace('.','. ')
                temp.append(w)
        new_text.append(' '.join(e for e in temp))
    return new_text

def rem_apostrophes(text):
    new_text = []
    for line in text:
        new_text.append(re.sub("'",'',line))
    return new_text
```

In [42]:
```
def Preprocessing(text):
    '''Combining all the functions'''
    pre_text = lowercase(text)
    pre_text = decontractions(pre_text)
    pre_text = rem_punctuations(pre_text)
    pre_text = rem_numbers(pre_text)
    pre_text = words_filter(pre_text)
    pre_text = multiple_fullstops(pre_text)
    pre_text = fullstops(pre_text)
    pre_text = multiple_spaces(pre_text)
    pre_text = separting_startg_words(pre_text)
    pre_text = rem_apostrophes(pre_text)
    return pre_text
```

In [43]:
```
Train_data['Findings'] = Preprocessing(Train_data['Findings'])
Test_data['Findings'] = Preprocessing(Test_data['Findings'])
CV_Data['Findings'] = Preprocessing(CV_Data['Findings'])
```

In [44]:
```
Train_data.head()
```

Out[44]:

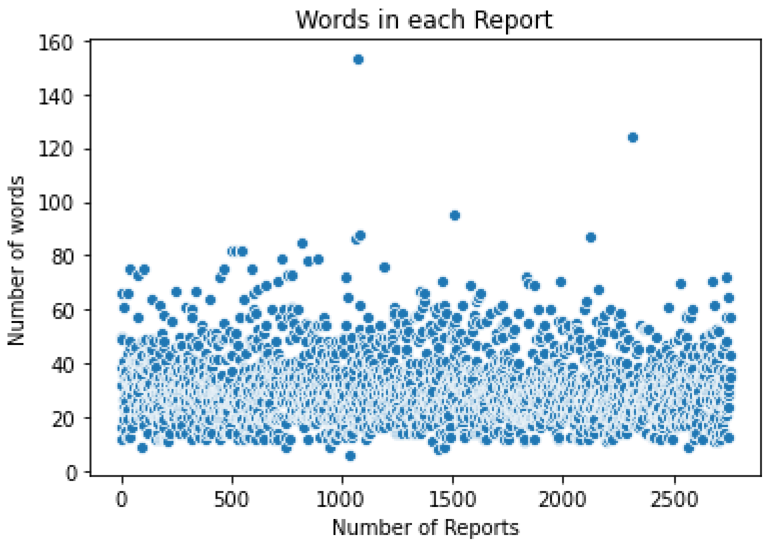
	Person_id	Image-1	Image-2	Findings
0	x ray data/CXR1_1_IM-0001_0	x ray data/CXR1_1_IM-0001-3001.png	x ray data/CXR1_1_IM-0001-4001.png	the cardiac silhouette and mediastinum size ar...
1	x ray data/CXR10_IM-0002_0	x ray data/CXR10_IM-0002-1001.png	x ray data/CXR10_IM-0002-2001.png	the cardiomediastinal silhouette within normal...
2	x ray data/CXR100_IM-0002_0	x ray data/CXR100_IM-0002-1001.png	x ray data/CXR100_IM-0002-2001.png	both lungs are clear and epanded . heart and ...
3	x ray data/CXR1000_IM-0003_0	x ray data/CXR1000_IM-0003-1001.png	x ray data/CXR1000_IM-0003-2001.png	there increased opacity within the right upper...
4	x ray data/CXR1000_IM-0003_1	x ray data/CXR1000_IM-0003-1001.png	x ray data/CXR1000_IM-0003-3001.png	there increased opacity within the right upper...

In [45]:
```
#finding number of words in each report
words = [len(i.split()) for i in Train_data['Findings'].values]
print(max(words))
```

```
153
```

```
In [46]: #plotting scatter plot for number of words in each report
         sns.scatterplot(range(Train_data.shape[0]), words)
         plt.xlabel('Number of Reports')
         plt.ylabel('Number of words')
         plt.title('Words in each Report')

Out[46]: Text(0.5, 1.0, 'Words in each Report')
```



Here we can see that majority of the reports contains 20 to 60 words.

```
In [47]: #finding number of words in train,cv,test data
         train_words = []
         for i in Train_data['Findings'].values:
             train_words.extend(i.split())
         test_words = []
         for i in Test_data['Findings'].values:
             test_words.extend(i.split())
         cv_words = []
         for i in CV_Data['Findings'].values:
             cv_words.extend(i.split())
         print('total number of words in train data',len(train_words))
         print('total number of words in test data',len(test_words))
         print('total number of words in cv data',len(cv_words))

         total number of words in train data 87458
         total number of words in test data 12521
         total number of words in cv data 18000
```

In [48]:
```
#finding unique words from total words
train_c= Counter(train_words)
test_c = Counter(test_words)
cv_c   = Counter(cv_words)

print('Number of Unique words in train data',len(train_c))
print('Number of Unique words in test data',len(test_c))
print('Number of Unique words in cv data',len(cv_c))
```

```
Number of Unique words in train data 1424
Number of Unique words in test data 735
Number of Unique words in cv data 804
```

In [49]:
```
#printing 50 most common words from train data
print(train_c.most_common(50))
```

```
[('.', 12558), ('the', 5102), ('no', 3647), ('are', 3457), ('normal', 2831),
('and', 2254), ('pleural', 1982), ('there', 1979), ('pneumothora', 1956), ('e
ffusion', 1817), ('heart', 1736), ('lungs', 1584), ('size', 1569), ('focal',
1407), ('within', 1270), ('clear', 1187), ('limits', 1178), ('pulmonary', 97
0), ('consolidation', 864), ('silhouette', 800), ('right', 769), ('mediastina
l', 686), ('airspace', 682), ('cardiomediastinal', 665), ('left', 641), ('acu
te', 574), ('lung', 566), ('with', 510), ('unremarkable', 507), ('disease', 4
91), ('stable', 489), ('spine', 481), ('mediastinum', 475), ('structures', 47
2), ('changes', 461), ('contours', 446), ('thoracic', 436), ('bony', 433),
('contour', 419), ('mild', 388), ('degenerative', 380), ('large', 373), ('see
n', 359), ('appear', 336), ('opacity', 333), ('osseous', 332), ('without', 33
1), ('calcified', 323), ('cardiac', 318), ('effusions', 311)]
```

In [50]:
```
#printing most common words from test data
print(test_c.most_common(50))
```

```
[('.', 1773), ('the', 706), ('no', 526), ('are', 501), ('normal', 410), ('an
d', 338), ('pleural', 304), ('pneumothora', 279), ('there', 274), ('heart', 2
67), ('effusion', 265), ('size', 233), ('lungs', 228), ('focal', 225), ('clea
r', 177), ('limits', 173), ('within', 163), ('pulmonary', 143), ('consolidati
on', 129), ('silhouette', 116), ('right', 104), ('cardiomediastinal', 103),
('mediastinal', 101), ('airspace', 100), ('lung', 89), ('stable', 86), ('lef
t', 82), ('changes', 77), ('with', 76), ('acute', 75), ('disease', 72), ('med
iastinum', 69), ('contour', 69), ('spine', 67), ('contours', 63), ('large', 6
2), ('thoracic', 60), ('without', 57), ('vascularity', 56), ('appear', 55),
('unremarkable', 55), ('seen', 53), ('degenerative', 52), ('for', 49), ('calc
ified', 49), ('bony', 47), ('effusions', 47), ('structures', 46), ('upper', 4
5), ('cardiac', 43)]
```

In [51]:
```
#printing 50 most common words from cv data
print(cv_c.most_common(50))
```

```
[('.', 2525), ('the', 1082), ('no', 737), ('are', 725), ('normal', 557), ('an
d', 440), ('pleural', 424), ('there', 407), ('pneumothora', 406), ('effusio
n', 385), ('heart', 337), ('lungs', 310), ('focal', 303), ('size', 294), ('li
mits', 265), ('within', 252), ('clear', 248), ('consolidation', 180), ('pulmo
nary', 177), ('silhouette', 176), ('airspace', 153), ('cardiomediastinal', 14
3), ('with', 141), ('right', 140), ('left', 139), ('mediastinal', 137), ('str
uctures', 110), ('changes', 106), ('stable', 105), ('lung', 105), ('spine', 1
04), ('acute', 103), ('disease', 102), ('mediastinum', 97), ('thoracic', 91),
('bony', 91), ('unremarkable', 90), ('degenerative', 83), ('without', 82),
('contours', 81), ('intact', 79), ('large', 75), ('cardiac', 72), ('contour',
72), ('osseous', 69), ('mild', 69), ('for', 67), ('opacity', 65), ('upper', 6
3), ('abnormality', 63)]
```

In [52]:
```
#common words between train ,test and cv
common_train_cv = train_c & cv_c &test_c
print(len(common_train_cv))
```

```
521
```

In [53]:
```
#printing 50 most common words present in all train,test,cv
common_train_cv.most_common(50)
```

Out[53]:
```
[('.', 1773),
 ('the', 706),
 ('no', 526),
 ('are', 501),
 ('normal', 410),
 ('and', 338),
 ('pleural', 304),
 ('pneumothora', 279),
 ('there', 274),
 ('heart', 267),
 ('effusion', 265),
 ('size', 233),
 ('lungs', 228),
 ('focal', 225),
 ('clear', 177),
 ('limits', 173),
 ('within', 163),
 ('pulmonary', 143),
 ('consolidation', 129),
 ('silhouette', 116),
 ('right', 104),
 ('cardiomediastinal', 103),
 ('mediastinal', 101),
 ('airspace', 100),
 ('lung', 89),
 ('stable', 86),
 ('left', 82),
 ('changes', 77),
 ('with', 76),
 ('acute', 75),
 ('disease', 72),
 ('mediastinum', 69),
 ('contour', 69),
 ('spine', 67),
 ('contours', 63),
 ('large', 62),
 ('thoracic', 60),
 ('without', 57),
 ('unremarkable', 55),
 ('vascularity', 54),
 ('seen', 53),
 ('degenerative', 52),
 ('for', 49),
 ('calcified', 49),
 ('appear', 47),
 ('bony', 47),
 ('effusions', 47),
 ('structures', 46),
 ('upper', 45),
 ('cardiac', 43)]
```

Here we can see that there are about 87,000 words in train data most of the words are repeated and we see that there are only 1424 unique words in train data and 735,804 in test and validation data respectively.And also we can see that most common words in all these sets are almost same.

```
In [54]: common = train_c & cv_c
         print(len(common))
```

```
701
```

```
In [55]: print('{0} % of train words present in cv data'.format(len(common)/len(train_c
         )*100))
```

```
49.22752808988764 % of train words present in cv data
```

```
In [56]: common_1 = train_c & test_c
         print(len(common_1))
```

```
655
```

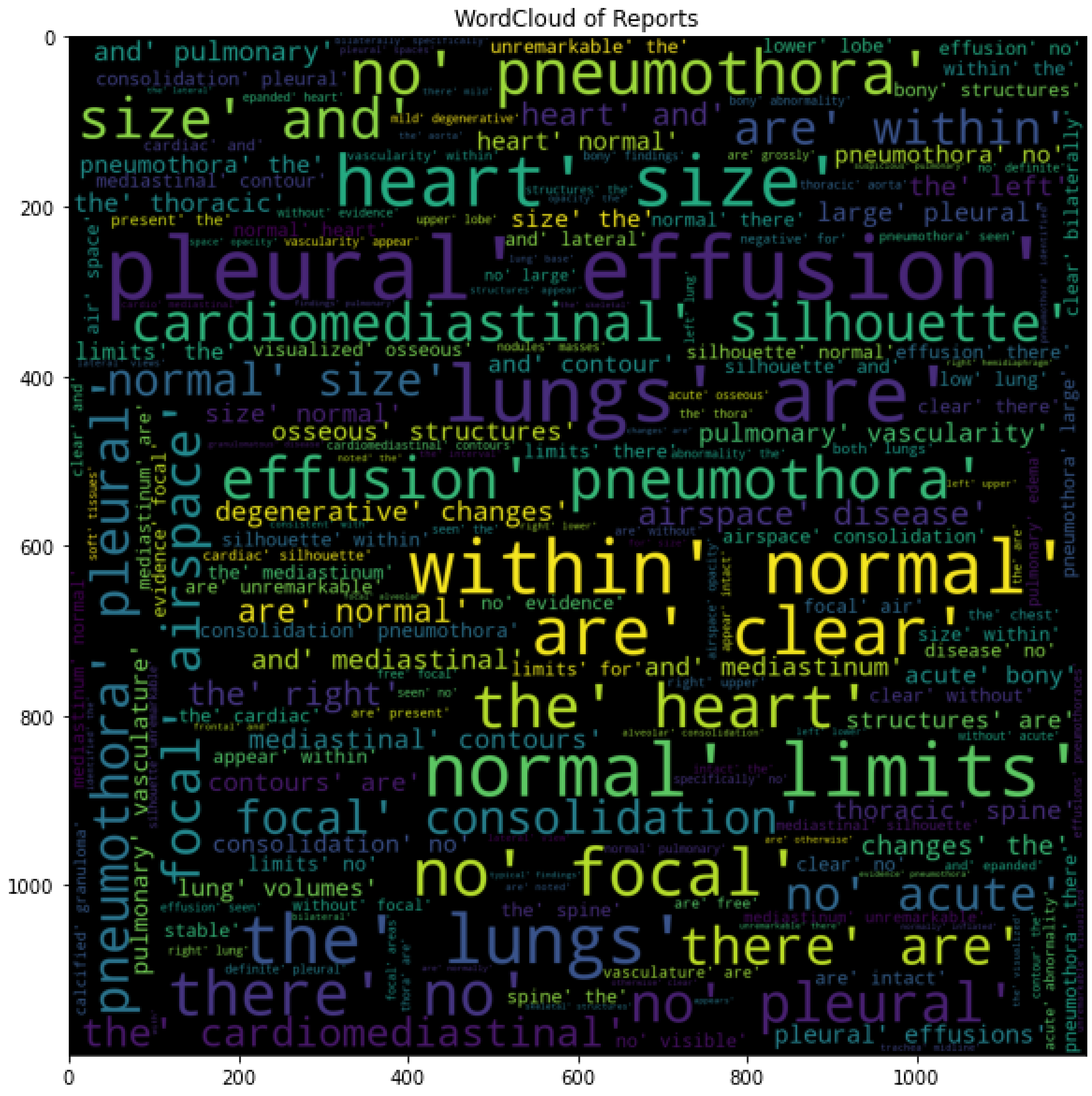
```
In [57]: print('{0} % of train words present in cv data'.format(len(common_1)/len(train
         _c)*100))
```

```
45.997191011235955 % of train words present in cv data
```

Here we can see that only 50% of the words that are present in validation data are present in train data. And only about 46% of the words that are present in test data are present in train data.

```
In [58]: words=[]
         for i in Train_data['Findings'].values:
             words.extend(i.split())
         w = WordCloud(height=1200, width=1200).generate(str(words))
         plt.figure(figsize=(10,10))
         plt.title('WordCloud of Reports')
         plt.imshow(w)

Out[58]: <matplotlib.image.AxesImage at 0x18f7df5fd68>
```



```
In [59]: #function for adding start of sentence and end of sequence in reports
         def add(x):
             return 'SOS' + ' ' + x + ' ' + 'EOS'
```

```
In [60]: Train_data['Findings'] = Train_data['Findings'].apply(lambda x : add(x))
         Test_data['Findings'] = Test_data['Findings'].apply(lambda x : add(x))
         CV_Data['Findings'] = CV_Data['Findings'].apply(lambda x : add(x))
```

In [61]:
```
#dumping data to csv files
Train_data.to_csv('Train_Data.csv', index=False)
Test_data.to_csv('Test_Data.csv', index=False)
CV_Data.to_csv('CV_Data.csv', index=False)
```